Correction for Delay and Dispersion of Contrast Bolus: A Comparison of Quantitative DSC Cerebral Perfusion and [^{15}O]-H_2O PET

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INTRODUCTION

Quantitative cerebral perfusion has been achieved via the Bookend technique [1,2] using dynamic susceptibility contrast (DSC) MRI and T_1 changes in normal white matter (WM) in relation to the changes in the blood pool in a single calibration slice, after contrast injection. Quantitative cerebral blood flow (qCBF), quantitative cerebral blood volume (qCBV) and mean transit time (MTT) measured by the Bookend technique have been proven reproducible, reliable and accurate [3]. However, in DSC perfusion imaging, delay and dispersion of the contrast bolus between the site of the arterial input function (AIF) and tissue curve measurement is known to reduce the accuracy of perfusion values [5-8]. Wu, et al. [5] proposed a time-shift insensitive technique by the use of a block-circulant matrix for singular value decomposition (SVD) deconvolution (cSVD), and Smith, et al. [6] presented a reformulation of SVD (rSVD) deconvolution approaches to account for arterial-tissue delay (ATD). While able to correct for the delay, the dispersion effect was still present with these methods. We propose a new correction model which accounts for both delay and dispersion. We validate our method through simulations and by direct comparison of MRI to positron emission tomography (PET), a recognized standard of reference for cerebral perfusion imaging [9] in patients with angiographically confirmed cerebrovascular occlusive disease (CVD).

MATERIALS AND METHODS

Dispersion Correction Model

We have developed a new dispersion model (Eq. [1]) which is a simplified version of the Willats, et al [8]'s effective residue function having both bolus arrival delay and MTT dependence. In our model, ΔBAT is the difference in bolus arrival time between the AIF and the tissue curve under consideration, A is an amplitude constant and β is a dispersion constant, characteristic of the cerebral vasculature system:

$$R_d(t,\Delta BAT) = \frac{A}{\Delta BAT + 1} e^{-\beta \frac{t}{\Delta BAT}} \qquad \textit{Eq. [1]}$$

The patient-specific dispersion model was determined by fitting a venous residue function to Eq. [1], using the venous ATD. A gamma-variate fit of the AIF was then convolved with the dispersion model with appropriate ATD for each voxel. The resulting AIFs deconvolved the corresponding C-T curves.

Computer Simulations

A simulated AIF was obtained using the standard simulation process described by Calamante, et al [7], and TR = 1 sec. Simulations were performed using standard SVD [10], rSVD [6], cSVD, and SVD with the proposed correction model (**bSVD**) across a range of MTT (6, 12 and 24 sec) and ATD (0 to 6 sec, with increments of TR) values. β=1.5 was used for dispersion, and T_{OFFSET} = -10xTR for rSVD [6].

in vivo Validation

Five patients with confirmed CVD were enrolled from an ongoing clinical trial at Washington University School of Medicine. Patients were scanned with the Bookend MR technique [3] at 3T (Trio, Siemens) and with [^{15}O]-H_2O PET [9]. All analysis was performed in MATLAB V7.8.0 (R2009a). ROIs were drawn on prompt (ΔBAT =0 to 1.5 s) and delayed (ΔBAT =1.5 to 9 s, resulting from vessel occlusion) areas for each patient. Pearson's correlations were computed to compare MR to PET cerebral blood flow (CBF) values in these ROIs, with (bSVD) and without (SVD) applying the proposed correction.

RESULTS/DISCUSSION

Fig. 1 shows that the **bSVD** method outperforms all other methods via simulations for MTT = 6 s. Table 1 shows that bSVD provides the most accurate qCBF values for short and long MTT values. bSVD correction effect was as large as 40% for all MTT values. Fig. 2 provides a visual comparison of the bSVD correction effect on the MR qCBF maps compared to PET. MR/PET CBF correlations improved due to the correction. Before correction (SVD): slope = 0.79, r = 0.60, and intercept = 11.7, and after correction (bSVD): slope = 0.91, r = 0.79, and intercept = 8.17. The measured MR qCBV values were not affected by the correction for all ROIs (Student's *t* test: p = 0.32 > 0.05 and r = 0.99), which is expected since the ATD/dispersion problem is inherent to the SVD deconvolution algorithm of the DSC analysis.

MTT (s)	SVD	rSVD	cSVD	**bSVD**
6	0.45 ± 0.18	0.43 ± 0.13	0.44 ± 0.14	**0.85 ± 0.02**
12	0.54 ± 0.18	0.53 ± 0.14	0.53 ± 0.16	**0.91 ± 0.01**
24	0.60 ± 0.17	0.60 ± 0.15	0.59 ± 0.17	**0.97 ± 0.01**

Table 1: *Accuracy of the different SVD techniques, computed as the mean ± standard deviation of CBF/True CBF over the entire ATD range shown in Figure 1, for 3 different MTT values.*

bSVD Provides More Accurate Quantitative Perfusion Values in a Setting of Delay and Dispersion

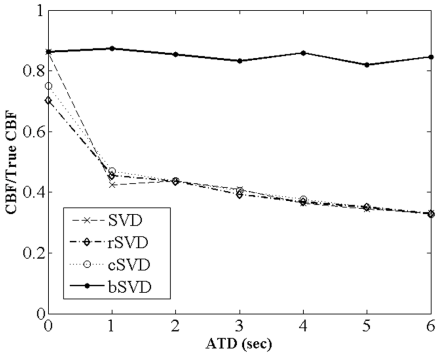

Figure 1: *Comparison of the accuracy of the 4 different deconvolution methods computed as the ratio of CBF computed by each method to the true CBF value used in the simulations, for MTT = 6 s.*

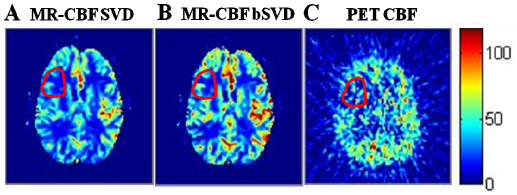

Figure 2: *A and B are MR quantitative CBF maps of a representative brain slice, obtained using SVD and bSVD, respectively. C is the corresponding PET CBF map. Mean CBF values in the ROI drawn on an area with delayed arrival (in red) were: 21.9±9.2, 25.8±13.8, and 30.7±17.8 ml/100 g/min, for A, B, and C, respectively.*

CONCLUSIONS

We have validated a correction model for delay and dispersion through computer simulations and *in vivo* comparison of MR and gold standard PET perfusion values. This model is valid for ATD > 0 (bolus arrival to tissue is greatly delayed with respect to the AIF), and future work will be aimed at correcting for ATD < 0 (due to AIF measurement near an occluded vessel).

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